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<input type="checkbox"/>	L5	(increas\$ or enhanc\$ or improv\$) near3 L4	460
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<input type="checkbox"/>	L3	sequence same L2	1201
<input type="checkbox"/>	L2	(increas\$ or enhanc\$ or improv\$) near3 L1	2495
<input type="checkbox"/>	L1	translat\$ near3 efficien\$	18253

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\*\*\*\*\* STN Columbus \*\*\*\*\*

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=> s l1 and sequence  
L2 3237 L1 AND SEQUENCE

=> s (improv? or increas? or enhanc? or regulat?) and l2  
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L4 20 L3 AND POLYRIBOSOM?

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L5 12 DUP REM L4 (8 DUPLICATES REMOVED)

=> d bib abs 1-  
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L5 ANSWER 1 OF 12 CAPLUS COPYRIGHT 2007 ACS ON STN  
AN 2006:117096 CAPLUS <<LOGINID::20070222>>  
DN 144:186045  
TI Nucleic acid sequences having translation \*\*\*enhancement\*\*\* activity  
and use  
IN Sawasaki, Tatsuya; Endo, Yaeta; Kamura, Nami  
PA Cellfree Sciences Co., Ltd., Japan  
SO U.S. Pat. Appl. Publ., 16 pp.  
CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2006029999	A1	20060209	US 2005-53594	20050208
JP 2006042676	A	20060216	JP 2004-227866	20040804
PRAI JP 2004-227866	A	20040804		

AB The present invention provides a polynucleotide comprising a nucleic acid  
\*\*\*sequence\*\*\* having an activity of \*\*\*regulating\*\*\* the  
\*\*\*translation\*\*\* \*\*\*efficiency\*\*\* of a template in a cell-free  
protein synthesis system and also provides a method for utilizing the  
same, etc. Protein synthesis is carried out by a translation template  
contg. a polynucleotide comprising a nucleic acid \*\*\*sequence\*\*\* which  
is to be an object to be selected, a \*\*\*polyribosome\*\*\* fraction is  
prepd. from the reaction soln. and a nucleic acid \*\*\*sequence\*\*\*  
bonding to ribosome is analyzed whereupon a selection is done.

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AN 2006272492 EMBASE <<LOGINID::20070222>>  
TI RNA helicase A is necessary for translation of selected messenger RNAs.  
AU Hartman T.R.; Qian S.; Bolinger C.; Fernandez S.; Schoenberg D.R.;  
Boris-Lawrie K.  
CS K. Boris-Lawrie, Center for Retrovirus Research, Department of Veterinary  
Biosciences, Ohio State University, Columbus, OH 43210, United States.  
boris-lawrie.1@osu.edu  
SO Nature Structural and Molecular Biology, (26 Jun 2006) Vol. 13, No. 6, pp.  
509-516.  
Refs: 50  
ISSN: 1545-9993 E-ISSN: 1545-9985 CODEN: NSMBCU

PUI N1092  
CY United States  
DT Journal; Article  
FS 022 Human Genetics  
029 Clinical Biochemistry  
LA English  
SL English  
ED Entered STN: 4 Aug 2006

Last Updated on STN: 4 Aug 2006  
AB RNA helicase A (RHA) is a highly conserved DEAD-box protein that activates  
transcription, modulates RNA splicing and binds the nuclear pore complex.  
The life cycle of typical mRNA involves RNA processing and translation  
after ribosome scanning of a relatively unstructured 5' untranslated  
region (UTR). The precursor RNAs of retroviruses and selected cellular  
genes harbor a complex 5' UTR and use a yet-to-be-identified host  
post-transcriptional effector to stimulate \*\*\*efficient\*\*\*  
\*\*\*translation\*\*\*. Here we show that RHA recognizes a structured  
5'-terminal post-transcriptional control element (PCE) of a retrovirus and  
the JUND growth-control gene. RHA interacts with PCE RNA in the nucleus  
and cytoplasm, facilitates \*\*\*polyribosome\*\*\* association and is  
necessary for its \*\*\*efficient\*\*\* \*\*\*translation\*\*\*. Our results  
reveal a previously unidentified role for RHA in translation and implicate  
RHA as an integrative effector in the continuum of gene expression from  
transcription to translation. .COPYRG. 2006 Nature Publishing Group.

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AN 2006260551 EMBASE <<LOGINID::20070222>>  
TI In vitro selection of translational \*\*\*regulatory\*\*\* elements.

AU Nagao I.; Obokata J.  
CS J. Obokata, Center for Gene Research, Nagoya University, Nagoya, 464-8602.

Japan. obokata@gene.nagoya-u.ac.jp

SO Analytical Biochemistry, (1 Jul 2006) Vol. 354, No. 1, pp. 1-7.

Refs: 38

ISSN: 0003-2697 E-ISSN: 1096-0309 CODEN: ANBCA2

PUI S 0003-2697(06)00243-0

CY United States

DT Journal; Article

FS 029 Clinical Biochemistry

LA English

SL English

ED Entered STN: 4 Jul 2006

Last Updated on STN: 4 Jul 2006

AB Untranslated regions (UTRs) of mRNAs carry various kinds of translational \*\*\*regulatory\*\*\* elements; however, our knowledge of them is still limited. We created an *in vitro* selection system that allows us to make a systematic enrichment of the sequences that alter \*\*\*translation\*\*\* \*\*\*efficiency\*\*\* (SESTRE) in any given mRNA and translation system. This method consists of the introduction of random nucleotide sequences into the UTRs of given mRNAs, followed by translation, size fractionation of the \*\*\*polyribosomes\*\*\*, and reverse transcription and PCR amplification (RT-PCR), with repeated cycles of these steps to enrich highly or poorly translatable mRNAs. With this experimental method, we examined how and where translational \*\*\*enhancer\*\*\* motifs emerge on mRNAs using the *in vitro* translation systems of wheat germ extract. The results indicate that the translational \*\*\*enhancers\*\*\* differentially emerge in response to the presence or absence of the 5' cap. Interestingly, the translational \*\*\*enhancers\*\*\* that activate cap-independent translation evolved more readily in the 3' UTR than in the 5' UTR in wheat germ extract. This SESTRE method should be a powerful tool with which to \*\*\*improve\*\*\* the \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* of given mRNAs in given translation systems and to investigate the structure-function relationship of eukaryotic mRNAs underlying translational control. COPYRIGHT. 2006 Elsevier Inc. All rights reserved.

L5 ANSWER 4 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN DUPLICATE 1

AN 2004168536 EMBASE <<LOGINID::20070222>>

TI Inhibition of Glutamate Receptor 2 Translation by a Polymorphic Repeat \*\*\*Sequence\*\*\* in the 5'-Untranslated Leaders.

AU Myers S.J.; Huang Y.; Genetta T.; Dingledine R.

CS R. Dingledine, Department of Pharmacology, Emory University School of Medicine, Atlanta, GA 30322, United States. rdingledine@pharm.emory.edu

SO Journal of Neuroscience, (7 Apr 2004) Vol. 24, No. 14, pp. 3489-3499.

Refs: 56

ISSN: 0270-6474 CODEN: JNRSDS

CY United States

DT Journal; Article

FS 002 Physiology

008 Neurology and Neurosurgery

029 Clinical Biochemistry

LA English

SL English

ED Entered STN: 13 May 2004

Last Updated on STN: 13 May 2004

AB Previous studies have identified multiple transcription initiation sites for the glutamate receptor 2 (GluR2) gene, resulting in a heterogeneous population of GluR2 transcripts *in vivo* that differ in the length of their 5'-untranslated leaders (5'-UTR). We designed a series of monocistronic and dicistronic GluR2 cDNA constructs that model the natural *in vivo* transcripts and investigated their \*\*\*translation\*\*\* \*\*\*efficiencies\*\*\* in rabbit reticulocyte lysates, *Xenopus* oocytes, and primary cultured neurons. Transcripts containing long 5' leaders (429 and 481 bases) were translated poorly compared with those with shorter leaders (341 or fewer bases). None of the five initiation codons in the 5'-UTR or the leader length per se were responsible for translation \*\*\*regulation\*\*\*. Rather, control of translation was mediated by a \*\*\*sequence\*\*\* containing a 34-42 nucleotide imperfect GU repeat predicted to form secondary structure *in vivo*. This translation suppression domain is included in some but not all rat and human GluR2 transcripts *in vivo*, depending on the site of transcription initiation. Rat cortex GluR2 transcripts that lack the translation suppression \*\*\*sequence\*\*\* were preferentially associated with \*\*\*polyribosomes\*\*\*. Furthermore, the GU-repeat cluster was found to be polymorphic in humans, raising the possibility that expansion or contraction of the GU-repeat cluster in certain populations might modify the level of GluR2 protein expression in neurons.

L5 ANSWER 5 OF 12 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2003:532764 CAPLUS <<LOGINID::20070222>>

DN 139:80165

TI Isolating nucleotide \*\*\*sequence\*\*\* \*\*\*regulating\*\*\* the \*\*\*translation\*\*\* \*\*\*efficiency\*\*\* in cell-free protein synthesis system

IN Endo; Yaeta; Sawasaki, Tatsuya

PA Japan

SO PCT Int. Appl., 89 pp.

CODEN: PIXXD2

DT Patent

LA Japanese

FAN.CNT 1

PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 2003056009 A1 20030710 WO 2002-JP13756 20021227  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MY, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG  
CA 2471667 A1 20030710 CA 2002-2471667 20021227  
AU 2002367144 A1 20030715 AU 2002-367144 20021227  
EP 1466972 A1 20041013 EP 2002-790919 20021227  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK  
JP 3701292 B2 20050928 JP 2003-556526 20021227  
US 2004248140 A1 20041209 US 2004-500346 20040729  
PRAI JP 2001-396941 A 20011227  
WO 2002-JP13756 W 20021227

AB A method of prep. a polynucleotide contg. a nucleotide \*\*\*sequence\*\*\* which \*\*\*regulate\*\*\* the \*\*\*translation\*\*\* \*\*\*efficiency\*\*\* of a template in a protein synthesis system, comprising (a) applying a template contg. one or more arbitrary nucleotide sequences to a protein synthesis reaction system, (b) after reacting, recovering a \*\*\*polyribosome\*\*\* fraction from the liq. reaction mixt., and (c) collecting a polynucleotide contg. the nucleotide \*\*\*sequence\*\*\* in the template from the \*\*\*polyribosome\*\*\* fraction; novel polynucleotides \*\*\*regulating\*\*\* the \*\*\*translation\*\*\* \*\*\*efficiency\*\*\* obtained by the above method; a method of synthesizing a protein with the use of a template contg. such a polynucleotide; and so on. Use of d. gradient centrifugation for collecting \*\*\*polyribosome\*\*\* fraction is claimed. Isolation of 27 57nt randomized sequences and 96 22nt randomized sequences are reported.

RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L5 ANSWER 6 OF 12 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

AN 2004:194748 BIOSIS <<LOGINID::20070222>>

DN PREV200400195307

TI Alteration of subcellular distribution of tyrosine hydroxylase (TH) mRNA in rat adrenal medulla and PC12 cells.

AU Xu, L. [Reprint Author]; Baoyong, S. [Reprint Author]; Tank, A. W. [Reprint Author]

CS Dept. of Pharmacol. and Physiology, Univ. of Rochester Med. Ctr., Rochester, NY, USA

SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 157.3. <http://sfn.scholarone.com>. e-file. Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA, November 08-12, 2003. Society of Neuroscience.

DT Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 14 Apr 2004

Last Updated on STN: 14 Apr 2004

AB Posttranscriptional mechanisms have been shown to be important in the \*\*\*regulation\*\*\* of tyrosine hydroxylase (TH) gene expression. In previous studies, we found that the muscarinic acetylcholine receptor agonist, bethanechol, induced TH mRNA but not TH protein in rat adrenal medulla. In contrast nicotine induced both TH mRNA and TH protein in rat adrenal medulla. Similarly it has been reported that a single immobilization leads to a large induction in adrenal TH mRNA but a very small induction in TH protein. In PC12 cells we have observed that treatment with phorbol ester or high K<sup>+</sup> leads to induction of TH mRNA without concomitant \*\*\*increase\*\*\* in TH protein. These observations suggest that TH gene expression is \*\*\*regulated\*\*\* at the translational level. In this study, we provide evidence for the possibility that TH mRNA \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* is changed due to alterations in the subcellular distribution of TH mRNA in rat adrenal medulla and PC12 cells. Subcellular fractions containing mRNP, monoribosomes and \*\*\*polyribosomes\*\*\* were separated using linear sucrose gradients. TH mRNA distribution in these fractions was determined using a semi-quantitative RT-PCR assay. We found that TH mRNA was localized mainly in \*\*\*polyribosomal\*\*\* and monoribosomal fractions and that the distribution of TH mRNA between these fractions was shifted by different stimuli. Our data are consistent with the hypothesis that the \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* of TH mRNA is \*\*\*regulated\*\*\* via differential subcellular distribution in response to activation of different signaling pathways. The detailed mechanisms including TH mRNA \*\*\*sequence\*\*\* and trans-acting factors responsible for this translational \*\*\*regulation\*\*\* are under investigation.

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AN 2002141977 EMBASE <<LOGINID::20070222>>

TI Replacement of the yeast TRP4 3' untranslated region by a hammerhead ribozyme results in a stable and efficiently exported mRNA that lacks a poly(A) tail.

AU Duvel K.; Valerius O.; Mangus D.A.; Jacobson A.; Braus G.H.  
CS G.H. Braus, Inst. of Microbiology and Genetics, Georg-August-University,  
Grisebachstr. 8, D-37077 Göttingen, Germany. gbraus@gwdg.de  
SO RNA, (2002) Vol. 8, No. 3, pp. 336-344.

Refs: 51

ISSN: 1355-8382 CODEN: RNARFU

CY United States

DT Journal; Article

FS 004 Microbiology

LA English

SL English

ED Entered STN: 2 May 2002

Last Updated on STN: 2 May 2002

AB The mRNA poly(A) tail serves different purposes, including the facilitation of nuclear export, mRNA stabilization, \*\*\*efficient\*\*\* translation\*\*\*, and, finally, specific degradation. The posttranscriptional addition of a poly(A) tail depends on \*\*\*sequence\*\*\* motifs in the 3' untranslated region (3' UTR) of the mRNA and a complex trans-acting protein machinery. In this study, we have replaced the 3' UTR of the yeast TRP4 gene with sequences encoding a hammerhead ribozyme that efficiently cleaves itself in vivo. Expression of the TRP4-ribozyme allele resulted in the accumulation of a nonpolyadenylated mRNA. Cells expressing the TRP4-ribozyme mRNA showed a reduced growth rate due to a reduction in Trp4p enzyme activity. The reduction in enzyme activity was not caused by inefficient mRNA export from the nucleus or mRNA destabilization. Rather, analyses of mRNA association with \*\*\*polyribosomes\*\*\* indicate that translation of the ribozyme-containing mRNA is impaired. This translational defect allows sufficient synthesis of Trp4p to support growth of trp4 cells, but is, nevertheless, of such magnitude as to activate the general control network of amino acid biosynthesis.

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AN 2000136717 EMBASE <<LOGINID::20070222>>

TI Post-transcriptional \*\*\*regulation\*\*\* of rat CYP2E1 expression: Role of CYP2E1 mRNA untranslated regions in control of \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* and message stability.

AU Kocarek T.A.; Zangar R.C.; Novak R.F.

CS R.F. Novak, Institute of Chemical Toxicology, Wayne State University, 2727 Second Avenue, Detroit, MI 48201, United States. r.novak@wayne.edu  
SO Archives of Biochemistry and Biophysics, (1 Apr 2000) Vol. 376, No. 1, pp. 180-190.

Refs: 27

ISSN: 0003-9861 CODEN: ABBIA4

CY United States

DT Journal; Article

FS 022 Human Genetics

029 Clinical Biochemistry

LA English

SL English

ED Entered STN: 4 May 2000

Last Updated on STN: 4 May 2000

AB Altered expression of hepatic CYP2E1 by xenobiotic or physiological stimuli is largely mediated through post-transcriptional mechanisms that may include altered CYP2E1 mRNA translation and/or protein degradation. Examination of the \*\*\*polyribosomal\*\*\* distribution of rat hepatic P450 mRNAs indicated that, whereas nearly all of the CYP2B, CYP3A, and CYP4A mRNAs were recovered in the polysomal fractions, indicating active translation, approximately 30-40% of CYP2E1 mRNA was not associated with polysomes and therefore not actively engaged in protein synthesis. To examine the CYP2E1 mRNA molecule for sequences that might affect its \*\*\*translational\*\*\* \*\*\*efficiency\*\*\*, a series of CYP2E1 recombinant RNAs (rcRNAs) with modified 5' or 3' untranslated regions (UTRs) was translated in vitro using the rabbit reticulocyte lysate system. Deletion of most of the CYP2E1 5' UTR, which was predicted to contain secondary structure, \*\*\*increased\*\*\* in vitro CYP2E1 protein synthesis. Polysomal distribution analyses of 5'-modified rcRNAs demonstrated that, as seen for hepatic CYP2E1 mRNA, a substantial fraction of each CYP2E1 rcRNA was not associated with polysomes. The polysomal distribution analyses of the CYP2E1 rcRNAs also confirmed that the observed changes in CYP2E1 protein synthesis were associated with altered ribosomal loading. Deletion of the poly(A) tail, and partial or complete deletion of the 3' UTR, decreased CYP2E1 protein synthesis. These changes in protein synthesis were accompanied by \*\*\*increased\*\*\* degradation of the CYP2E1 rcRNAs. Incubation with translational inhibitors, but not \*\*\*increased\*\*\* levels of RNase inhibitor, decreased the degradation of the rcRNAs during in vitro translation. In conclusion, these studies suggest that secondary structure in the 5' UTR of CYP2E1 mRNA is at least partially responsible for the inefficient translation of this mRNA. The poly(A) tail and sequences contained within the 3' UTR appear to be important for protecting CYP2E1 mRNA from RNase activity associated with the translation machinery. (C) 2000 Academic Press.

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DUPLICATE 2

AN 96153939 EMBASE <<LOGINID::20070222>>

DN 1996153939

TI \*\*\*Regulation\*\*\* of gene expression for translation initiation factor eIF-2.alpha.: Importance of the 3' untranslated region.

AU Miyamoto S.; Chiorini J.A.; Urcelay E.; Safer B.

CS Molecular Hematology Branch, Section Protein and RNA Biosynthesis, NHLBI,

10 Center Dr MSC 1654, Bethesda, MD 20892-1654, United States  
SO Biochemical Journal, (1996) Vol. 315, No. 3, pp. 791-798.

ISSN: 0264-6021 CODEN: BIJOAK

CY United Kingdom

DT Journal; Article

FS 022 Human Genetics

029 Clinical Biochemistry

LA English

SL English

ED Entered STN: 4 Jun 1996

Last Updated on STN: 4 Jun 1996

AB Gene expression of the  $\alpha$ -subunit of eukaryotic initiation factor-2 (eIF-2.alpha.), involves transcriptional and post-transcriptional mechanisms. eIF-2.alpha. is a single-copy gene expressing two mRNAs, 1.6 and 4.2 kb in size. Cloning and sequencing of the cDNA for the 4.2 kb mRNA revealed that it is the result of alternative polyadenylation site selection. Four polyadenylation sites were identified within the 3' untranslated region (UTR) of eIF-2.alpha., only two of which are normally utilized in human and mouse tissues. A functional role for the extended 3' UTR was assessed by comparing the translatability and stability of the 1.6 and kb mRNAs. Both the 1.6 and 4.2 kb transcripts could be translated in vitro and were identified in vivo as being distributed on large \*\*\*polyribosomes\*\*\*. This indicates that both mRNAs are \*\*\*efficiently\*\*\* \*\*\*translated\*\*\*. Stability studies showed that in activated T-cells the 4.2 kb mRNA was more stable than the 1.6 kb mRNA. Polyadenylation site selection and mRNA stability differ for the two mRNAs of eIF-2.alpha.. These activities might be modulated by \*\*\*sequence\*\*\* elements contained within the untranslated regions of the eIF-2.alpha. gene.

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AN 92134180 EMBASE <<LOGINID::20070222>>

DN 1992134180

TI The iron \*\*\*regulatory\*\*\* region of ferritin mRNA is also a positive control element for iron-independent translation.

AU Dix D.J.; Lin P.-N.; Kimata Y.; Theil E.C.

CS Department of Biochemistry, North Carolina State University, Raleigh, NC 27695-7622, United States

SO Biochemistry, (1992) Vol. 31, No. 10, pp. 2818-2822.

ISSN: 0006-2960 CODEN: BJCHAW

CY United States

DT Journal; Article

FS 022 Human Genetics

LA English

SL English

ED Entered STN: 24 May 1992

Last Updated on STN: 24 May 1992

AB The iron \*\*\*regulatory\*\*\* element (IRE) in the 5'-untranslated region of ferritin mRNA interacts with a specific \*\*\*regulator\*\*\* protein (P-90, IRE-BP, or FRP) to block translation. High cellular iron changes the IRE/P-90 interaction to relax the translational block and allow \*\*\*polyribosome\*\*\* formation. We now show that the IRE and base-paired flanking regions also \*\*\*enhance\*\*\* translation in the absence of P-90, explaining the high \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* of deregulated ferritin mRNA observed previously. The effect of the IRE on \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* was examined by comparing four sets of mRNAs: (1) +/-IRE in animal (frog) ferritin, \*\*\*regulated\*\*\* translationally by iron in vivo; (2) +/-animal IRE fused with plant (soybean) ferritin, \*\*\*regulated\*\*\* transcriptionally by iron in vivo; (3) repositioned IRE in animal ferritin; (4) mutated IRE in animal ferritin with G16A substitution, which decreases P-90 binding (negative control). The IRE region \*\*\*increased\*\*\* \*\*\*translational\*\*\* \*\*\*efficiency\*\*\* of both the animal ferritin and the heterologous IRE/soybean ferritin fusion mRNAs; the effect was observed in cell-free translation systems from either plants (wheat germ) or animals (rabbit reticulocyte). Repositioning the IRE further from the 5' cap eliminated positive control of translation. The single base mutation had no effect, indicating that positive and negative translational control involves different sections of the IRE region. Thus, the IRE region in ferritin mRNA encodes both positive translational control and, when combined with the \*\*\*regulator\*\*\* protein P-90, negative translational control.

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DUPLICATE 3

AN 90349590 EMBASE <<LOGINID::20070222>>

DN 1990349590

TI Translation of the Saccharomyces cerevisiae tcm1 gene in the absence of a 5'-untranslated leader.

AU Maicas E.; Shago M.; Friesen J.D.

CS Hospital for Sick Children, 555 University Avenue, Toronto, Ont., Canada

SO Nucleic Acids Research, (1990) Vol. 18, No. 19, pp. 5823-5828.

ISSN: 0305-1048 CODEN: NARHAD

CY United Kingdom

DT Journal; Article

FS 004 Microbiology

LA English

SL English

ED Entered STN: 13 Dec 1991

Last Updated on STN: 13 Dec 1991

AB The role of eukaryotic 5'-untranslated messenger RNA leaders is not entirely clear, since they share little \*\*\*sequence\*\*\* similarity among each other. The importance of the leader in determining the

\*\*\*efficiency\*\*\* of \*\*\*translation\*\*\* initiation was addressed here by examining the \*\*\*polynibosome\*\*\* distribution of several leader-deletion alleles of the yeast tcm1 gene (coding for ribosomal protein L3). Shortening of this 22-nucleotide leader, or complete removal of it (the first nucleotide of the mRNA becoming the A of the translation initiation codon AUG) permitted translation, albeit reduced. Further deletion of as few as the first two nucleotides of the initiation codon leads to a substantial reduction in ribosome loading, which is compatible with inefficient initiation at the next downstream, out-of-frame, AUG triplet. A second measure of translation initiation was obtained by assaying qualitatively for the production of biologically active L3 protein using growth-resistance to trichodermin. This experiment indicates that ribosomes can recognize the correct initiation codon even in the complete absence of a leader. We conclude that the 5'-untranslated leader of the yeast tcm1 gene is not essential for accurate translation initiation, but \*\*\*enhances\*\*\* its efficiency.

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AN 89210656 EMBASE <<LOGINID::20070222>>

DN 1989210656

TI Cap-independent translation of mRNA conferred by encephalomyocarditis virus 5' \*\*\*sequence\*\*\* \*\*\*improves\*\*\* the performance of the vaccinia virus/bacteriophage T7 hybrid expression system.

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SO Proceedings of the National Academy of Sciences of the United States of America, (1989) Vol. 86, No. 16, pp. 6126-6130. .  
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CY United States

DT Journal

FS 029 Clinical Biochemistry

047 Virology

LA English

SL English

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AB A recombinant vaccinia virus that directs the synthesis of bacteriophage T7 RNA polymerase provides the basis for the expression of genes that are \*\*\*regulated\*\*\* by T7 promoters in mammalian cells. The T7 transcripts, which account for as much as 30% of the total cytoplasmic RNA at 24 hr after infection, are largely uncapped. To \*\*\*improve\*\*\* the translatability of the uncapped RNA, the encephalomyocarditis virus (EMCV) untranslated region (UTR) was inserted between the T7 promoter and the chloramphenicol acetyltransferase (CAT) gene. Experiments with a reticulocyte extract demonstrated that the EMCV UTR conferred \*\*\*efficient\*\*\* and cap-independent \*\*\*translatability\*\*\* to CAT RNA synthesized in vitro by T7 RNA polymerase. In cells infected with recombinant vaccinia viruses containing the T7 promoter- \*\*\*regulated\*\*\* CAT gene, the EMCV UTR \*\*\*increased\*\*\* the amount of CAT RNA on \*\*\*polynibosomes\*\*\*. The \*\*\*polynibosome\*\*\*-derived CAT RNA, which contained the EMCV UTR, was translated in vitro in a cap-independent fashion as well. Use of the EMCV UTR significantly \*\*\*enhanced\*\*\* the vaccinia/T7 hybrid expression system as it resulted in a 4- to 7-fold \*\*\*increase\*\*\* in total CAT activity. A further .5meq.2-fold \*\*\*improvement\*\*\* was achieved by incubating the cells in hypertonic medium, which favors the translation of uncapped picornavirus RNA over cellular mRNAs. With this newly modified expression system, CAT was the predominant protein synthesized by infected cells and within 24 hr accounted for >10% of the total cell protein.

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